

SEQUENCE LISTING

<110> CHOI, YANG-DO
CHEONG, JONG-JOO
LEE, JONG-SEOB
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SEO, HAK-SOO
KOO, YEON-JONG

<120> GENES FOR S-ADENOSYL L-METHIONINE: JASMONIC ACID CARBOXYL METHYLTRANSFERASE AND A METHOD FOR THE DEVELOPMENT OF PATHOGEN- AND STRESS-RESISTANT PLANTS USING THE GENES

<130> 058333/0112

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<150> PCT/KR01/00953
<151> 2001-06-05

<160> 8

<170> PatentIn Ver. 2.1

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<213> Arabidopsis thaliana

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<221> CDS

<222> (15)...(1181)

<223> open reading frame for JMT

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aac ggg gaa aca agt tat gcc aag aac tcc acc gct cag agc aac ata	98
Asn Gly Glu Thr Ser Tyr Ala Lys Asn Ser Thr Ala Gln Ser Asn Ile	
15 20 25	

ata tct cta ggc aga aga gta atg gac gag gcc ttg aag aag tta atg	146
Ile Ser Leu Gly Arg Arg Val Met Asp Glu Ala Leu Lys Lys Leu Met	
30 35 40	

atg agc aat tca gag att tcg agc att gga atc gcc gac tta ggc tgc	194
Met Ser Asn Ser Glu Ile Ser Ser Ile Gly Ile Ala Asp Leu Gly Cys	
45 50 55 60	

tcc tcc ggt ccg aac agt ctc ttg tcc atc tcc aac ata gtt gac acg	242
Ser Ser Gly Pro Asn Ser Leu Leu Ser Ile Ser Asn Ile Val Asp Thr	
65 70 75	

atc cac aac ttg tgt cct gac ctc gac cgt cca gtc cct gag ctc aga	290
Ile His Asn Leu Cys Pro Asp Leu Asp Arg Pro Val Pro Glu Leu Arg	
80 85 90	

gtc tct ctc aac gac ctc cct agc aat gac ttc aac tac ata tgt gct	338
Val Ser Leu Asn Asp Leu Pro Ser Asn Asp Phe Asn Tyr Ile Cys Ala	
95 100 105	

tct ttg cca gag ttt tac gac cgg gtt aat aat aac aag gag ggt tta	386
Ser Leu Pro Glu Phe Tyr Asp Arg Val Asn Asn Lys Glu Gly Leu	
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ggg ttc ggt cgt gga gga gaa tcg tgt ttt gtg tcg gcc gtc cca	434
Gly Phe Gly Arg Gly Gly Glu Ser Cys Phe Val Ser Ala Val Pro	
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ggt tcg ttc tac gga cgt ttg ttt cct cgc cgg agc ctt cac ttt gtg	482
Gly Ser Phe Tyr Gly Arg Leu Phe Pro Arg Arg Ser Leu His Phe Val	
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cat tct tct tct agt tta cat tgg ttg tct cag gtt cca tgt cgt gag	530
His Ser Ser Ser Leu His Trp Leu Ser Gln Val Pro Cys Arg Glu	
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gcg gag aag gaa gac agg aca ata aca gct gat tta gaa aac atg ggg	578
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175 180 185	

aaa ata tac ata tca aag aca agt cct aag agt gca cat aaa gct tat	626
Lys Ile Tyr Ile Ser Lys Thr Ser Pro Lys Ser Ala His Lys Ala Tyr	
190 195 200	
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Ala Leu Gln Phe Gln Thr Asp Phe Leu Val Phe Leu Arg Ser Arg Ser	
205 210 215 220	
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Glu Glu Leu Val Pro Gly Gly Arg Met Val Leu Ser Phe Leu Gly Arg	
225 230 235	
 aga tca ctg gat ccc aca acc gaa gag agt tgc tat caa tgg gaa ctc	770
Arg Ser Leu Asp Pro Thr Thr Glu Glu Ser Cys Tyr Gln Trp Glu Leu	
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Leu Ala Gln Ala Leu Met Ser Met Ala Lys Glu Gly Ile Ile Glu Glu	
255 260 265	
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Glu Lys Ile Asp Ala Phe Asn Ala Pro Tyr Tyr Ala Ala Ser Ser Glu	
270 275 280	
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Glu Leu Lys Met Val Ile Glu Lys Glu Gly Ser Phe Ser Ile Asp Arg	
285 290 295 300	
 ctt gag ata agt ccg att gat tgg gaa ggt ggg agt atc agt gag gag	962
Leu Glu Ile Ser Pro Ile Asp Trp Glu Gly Ser Ile Ser Glu Glu	
305 310 315	
 agt tat gac ctt gca ata agg tcc aaa ccc gaa gcc cta gct agt ggc	1010
Ser Tyr Asp Leu Ala Ile Arg Ser Lys Pro Glu Ala Leu Ala Ser Gly	
320 325 330	
 cga aga gtg tct aat acc ata aga gct gtg gtc gag ccg atg cta gaa	1058
Arg Arg Val Ser Asn Thr Ile Arg Ala Val Val Glu Pro Met Leu Glu	
335 340 345	
 cct act ttc ggt gaa aat gtg atg gac gag ctt ttt gaa agg tat gca	1106
Pro Thr Phe Gly Glu Asn Val Met Asp Glu Leu Phe Glu Arg Tyr Ala	
350 355 360	
 aag atc gtg gga gag tac ttc tat gta agc tcg cca cga tac gct att	1154
Lys Ile Val Gly Glu Tyr Phe Tyr Val Ser Ser Pro Arg Tyr Ala Ile	
365 370 375 380	
 gtt att ctt tcg ctc gtt aga acc ggt tgatcggtt ataacatatg	1201
Val Ile Leu Ser Leu Val Arg Thr Gly	
385	
 ccaatataca tgtctttggg cctacaatga catgatttg tagtttcta atcaagcata	1261
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ctttttttt tttcttcatt tacggtagac ctatagtatt aaaacaaata gaatcagctg	1381

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 Arg Arg Val Met Asp Glu Ala Leu Lys Lys Leu Met Met Ser Asn Ser
 35 40 45
 Glu Ile Ser Ser Ile Gly Ile Ala Asp Leu Gly Cys Ser Ser Gly Pro
 50 55 60
 Asn Ser Leu Leu Ser Ile Ser Asn Ile Val Asp Thr Ile His Asn Leu
 65 70 75 80
 Cys Pro Asp Leu Asp Arg Pro Val Pro Glu Leu Arg Val Ser Leu Asn
 85 90 95
 Asp Leu Pro Ser Asn Asp Phe Asn Tyr Ile Cys Ala Ser Leu Pro Glu
 100 105 110
 Phe Tyr Asp Arg Val Asn Asn Asn Lys Glu Gly Leu Gly Phe Gly Arg
 115 120 125
 Gly Gly Gly Glu Ser Cys Phe Val Ser Ala Val Pro Gly Ser Phe Tyr
 130 135 140
 Gly Arg Leu Phe Pro Arg Arg Ser Leu His Phe Val His Ser Ser Ser
 145 150 155 160
 Ser Leu His Trp Leu Ser Gln Val Pro Cys Arg Glu Ala Glu Lys Glu
 165 170 175
 Asp Arg Thr Ile Thr Ala Asp Leu Glu Asn Met Gly Lys Ile Tyr Ile
 180 185 190
 Ser Lys Thr Ser Pro Lys Ser Ala His Lys Ala Tyr Ala Leu Gln Phe
 195 200 205
 Gln Thr Asp Phe Leu Val Phe Leu Arg Ser Arg Ser Glu Glu Leu Val
 210 215 220
 Pro Gly Gly Arg Met Val Leu Ser Phe Leu Gly Arg Arg Ser Leu Asp
 225 230 235 240
 Pro Thr Thr Glu Glu Ser Cys Tyr Gln Trp Glu Leu Leu Ala Gln Ala
 245 250 255

Leu Met Ser Met Ala Lys Glu Gly Ile Ile Glu Glu Glu Lys Ile Asp
 260 265 270

Ala Phe Asn Ala Pro Tyr Tyr Ala Ala Ser Ser Glu Glu Leu Lys Met
 275 280 285

Val Ile Glu Lys Glu Gly Ser Phe Ser Ile Asp Arg Leu Glu Ile Ser
 290 295 300

Pro Ile Asp Trp Glu Gly Ser Ile Ser Glu Glu Ser Tyr Asp Leu
 305 310 315 320

Ala Ile Arg Ser Lys Pro Glu Ala Leu Ala Ser Gly Arg Arg Val Ser
 325 330 335

Asn Thr Ile Arg Ala Val Val Glu Pro Met Leu Glu Pro Thr Phe Gly
 340 345 350

Glu Asn Val Met Asp Glu Leu Phe Glu Arg Tyr Ala Lys Ile Val Gly
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Glu Tyr Phe Tyr Val Ser Ser Pro Arg Tyr Ala Ile Val Ile Leu Ser
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Leu Val Arg Thr Gly
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: 5' primer for
 PCR of JMT gene

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<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: 3' primer for
 PCR of JMT gene

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<210> 6

<211> 359

<212> PRT

<213> Clarkia breweri

<400> 6

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Lys	Pro	Ile	Thr	Glu	Ala	Ala	Ile	Thr	Ala	Leu	Tyr	Ser	Gly	Asp	Thr
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Leu	Asn	Ala	Tyr	Tyr	Lys	Gln	Phe	Gln	Glu	Asp	His	Ala	Leu	Phe	Leu
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Arg	Cys	Arg	Ala	Gln	Glu	Val	Val	Pro	Gly	Gly	Arg	Met	Val	Leu	Thr
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Ile	Leu	Gly	Arg	Arg	Ser	Glu	Asp	Arg	Ala	Ser	Thr	Glu	Cys	Cys	Leu
		210			215				220						
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Leu	Ile	Glu	Glu	Glu	Lys	Met	Asp	Lys	Phe	Asn	Ile	Pro	Gln	Tyr	Thr
		245			250			255							
Pro	Ser	Pro	Thr	Glu	Val	Glu	Ala	Glu	Ile	Leu	Lys	Glu	Gly	Ser	Phe
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		275			280			285							

Lys Asp Gly Asp Gly Gly Ser Val Glu Glu Glu Gly Tyr Asn Val
290 295 300

Ala Arg Cys Met Arg Ala Val Ala Glu Pro Leu Leu Leu Asp His Phe
305 310 315 320

Gly Glu Ala Ile Ile Glu Asp Val Phe His Arg Tyr Lys Leu Leu Ile
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<211> 48

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<223> Description of Artificial Sequence: Synthetic
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<222> (1)..(48)

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<211> 16

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
peptide

<400> 8

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